

EXHIBIT 7

PART 1 OF 2



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(54) **NUCLEIC ACID READING AND ANALYSIS SYSTEM**

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25.32

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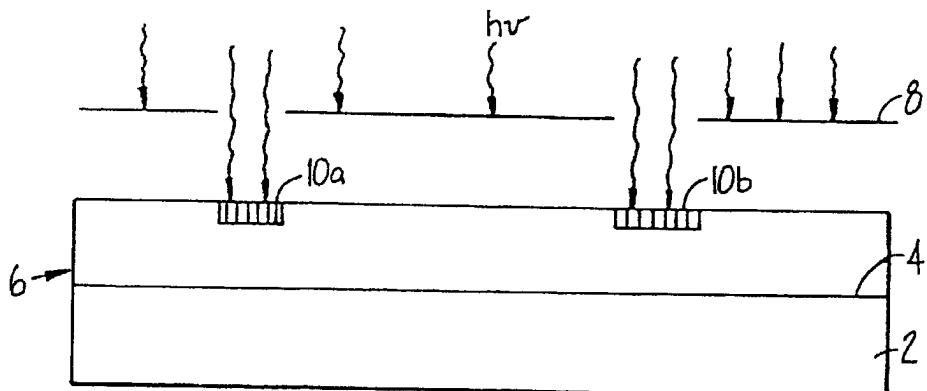
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(57) **ABSTRACT**

A method and apparatus for preparation of a substrate containing a plurality of sequences. Photoremovable groups are attached to a surface of a substrate. Selected regions of the substrate are exposed to light so as to activate the selected areas. A monomer, also containing a photoremovable group, is provided to the substrate to bind at the selected areas. The process is repeated using a variety of monomers such as amino acids until sequences of a desired length are obtained. Detection methods and apparatus are also disclosed.

53 Claims, 22 Drawing Sheets



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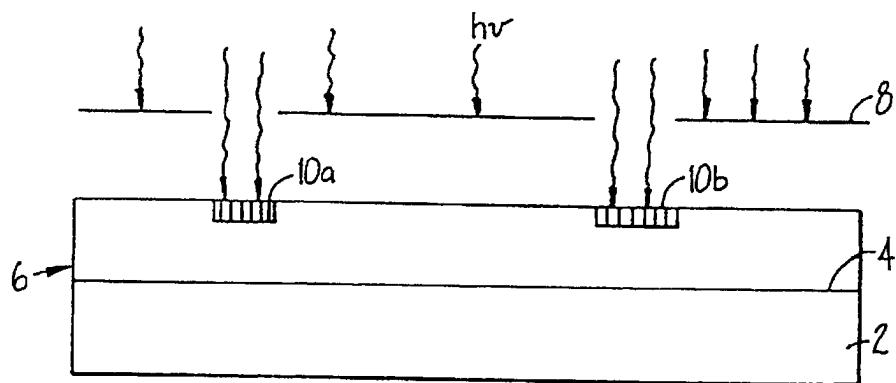


FIG. 1.

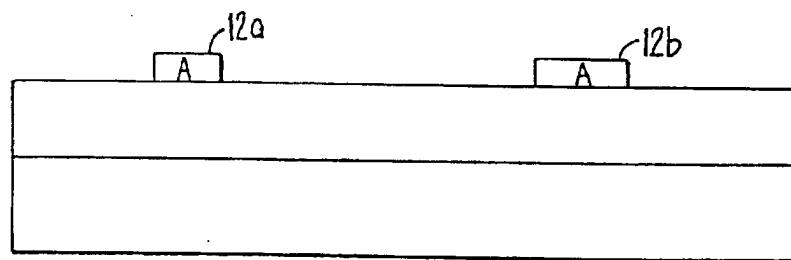


FIG. 2.

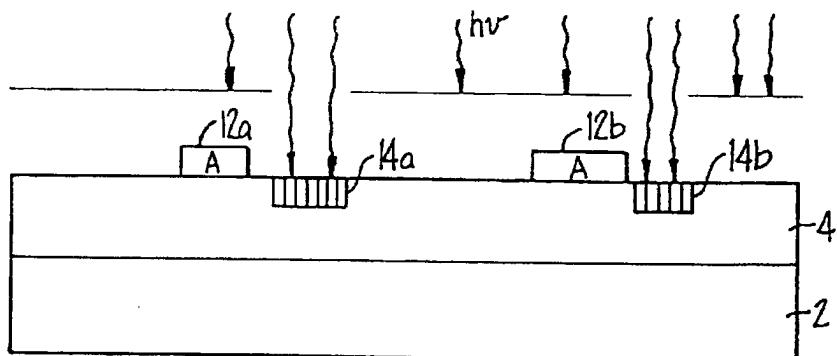


FIG. 3.

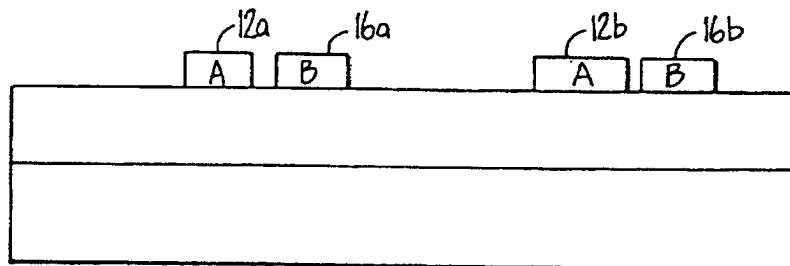


FIG. 4.

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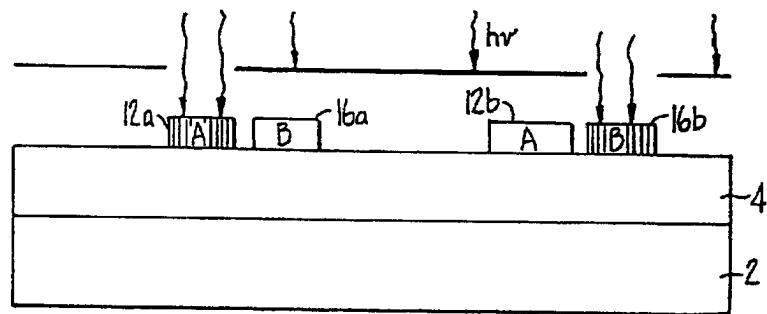


FIG. 5.

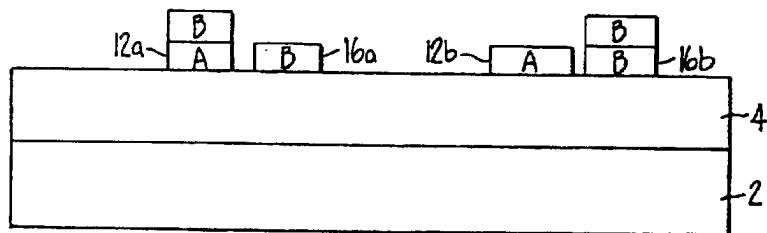


FIG. 6.

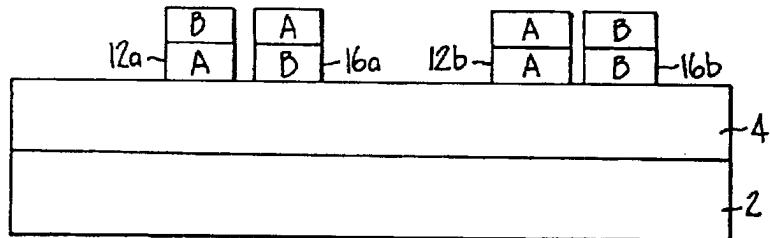


FIG. 7.

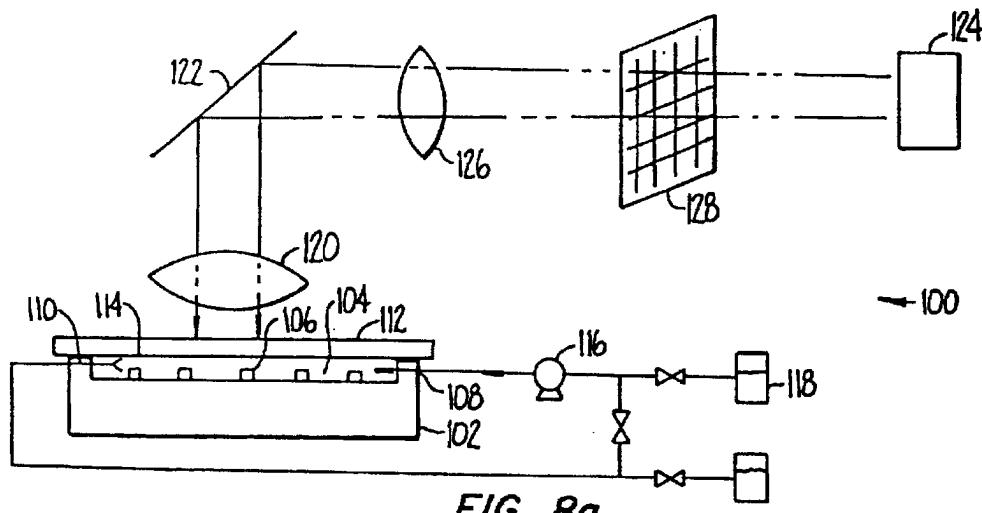


FIG. 8a.

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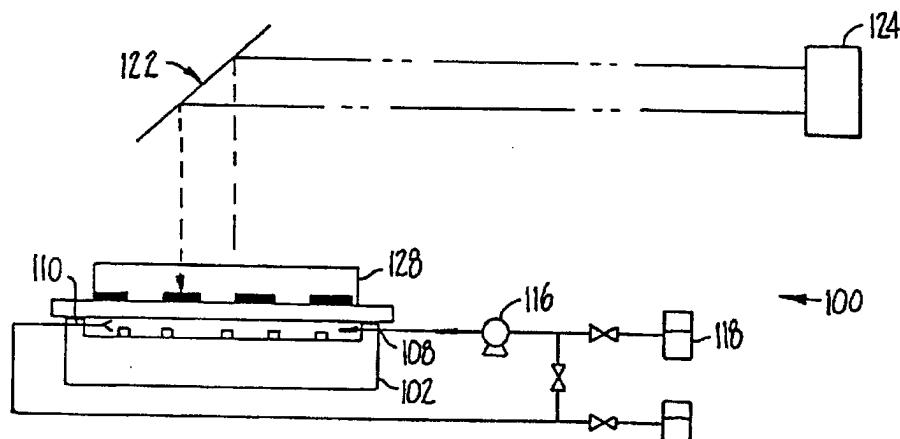


FIG. 8b.

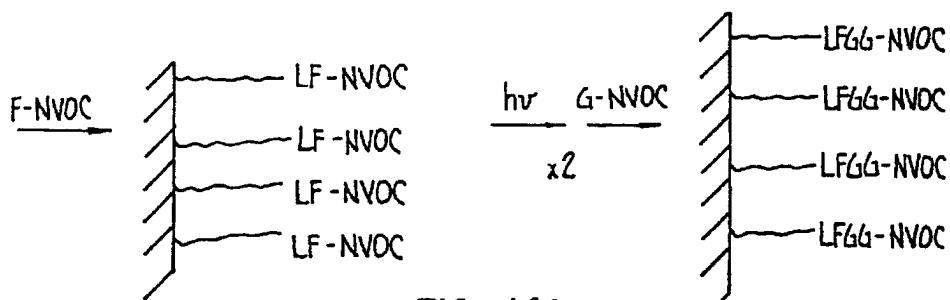
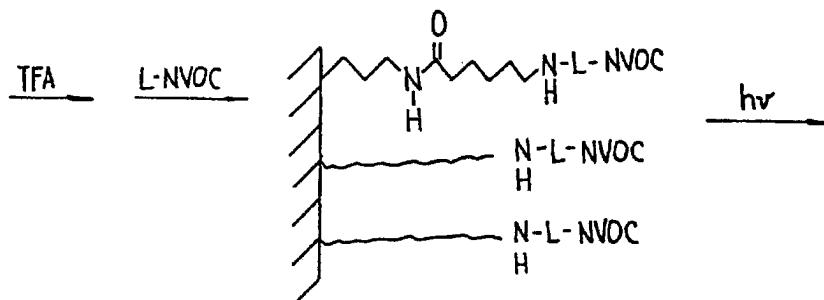
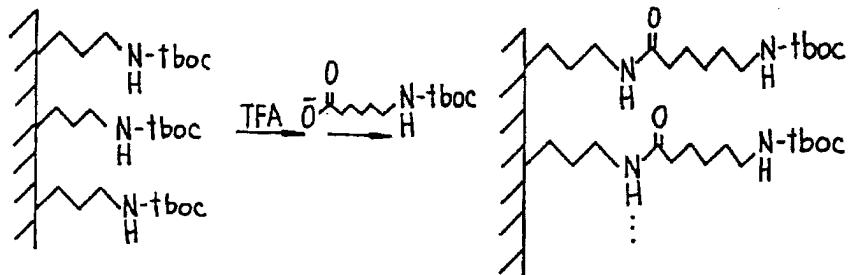


FIG. 14A.

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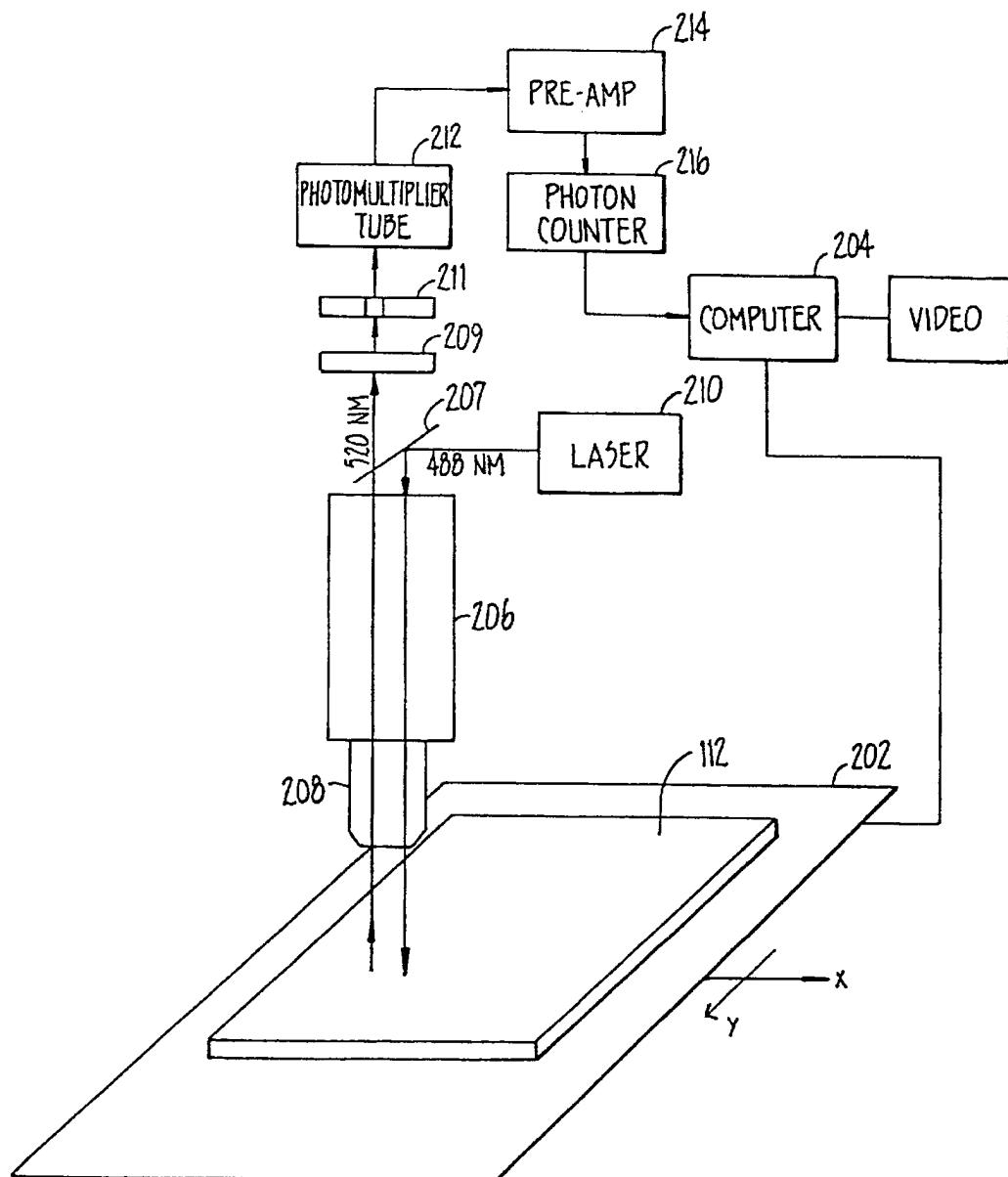


FIG. 9.

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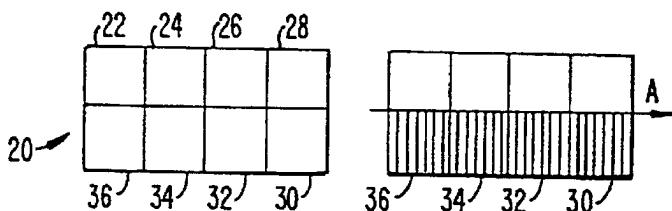


FIG. 10A.

FIG. 10B.

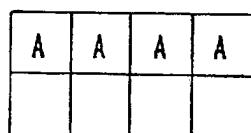


FIG. 10C.

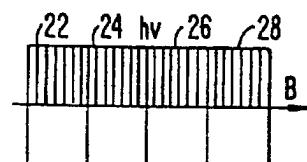


FIG. 10D.

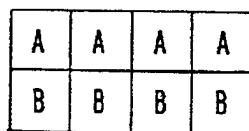


FIG. 10E.

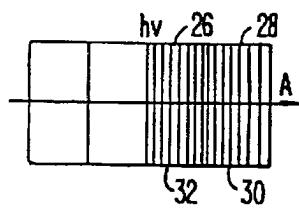


FIG. 10F.

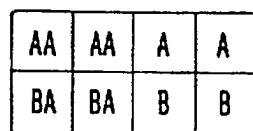


FIG. 10G.

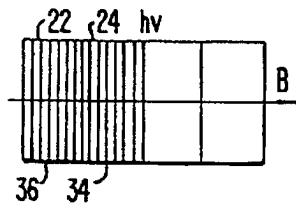


FIG. 10H.

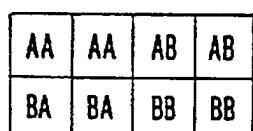


FIG. 10I.

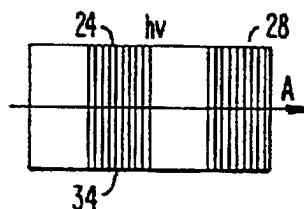


FIG. 10J.

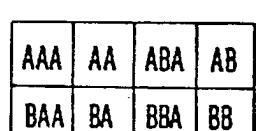


FIG. 10K.

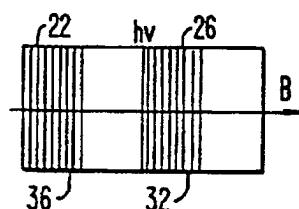


FIG. 10L.

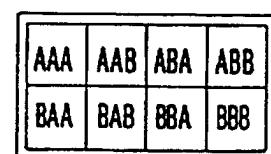


FIG. 10M.

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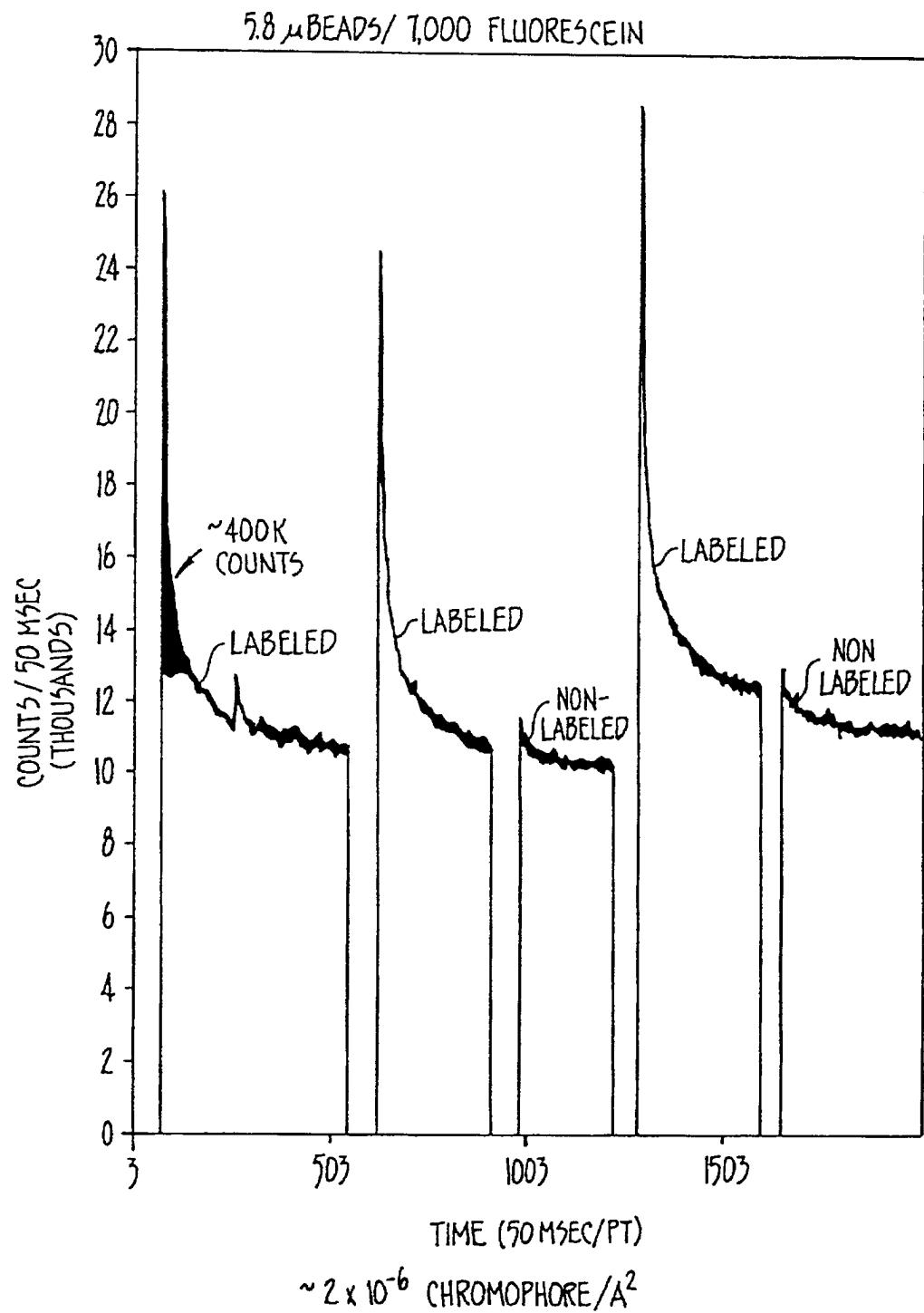


FIG. II A.

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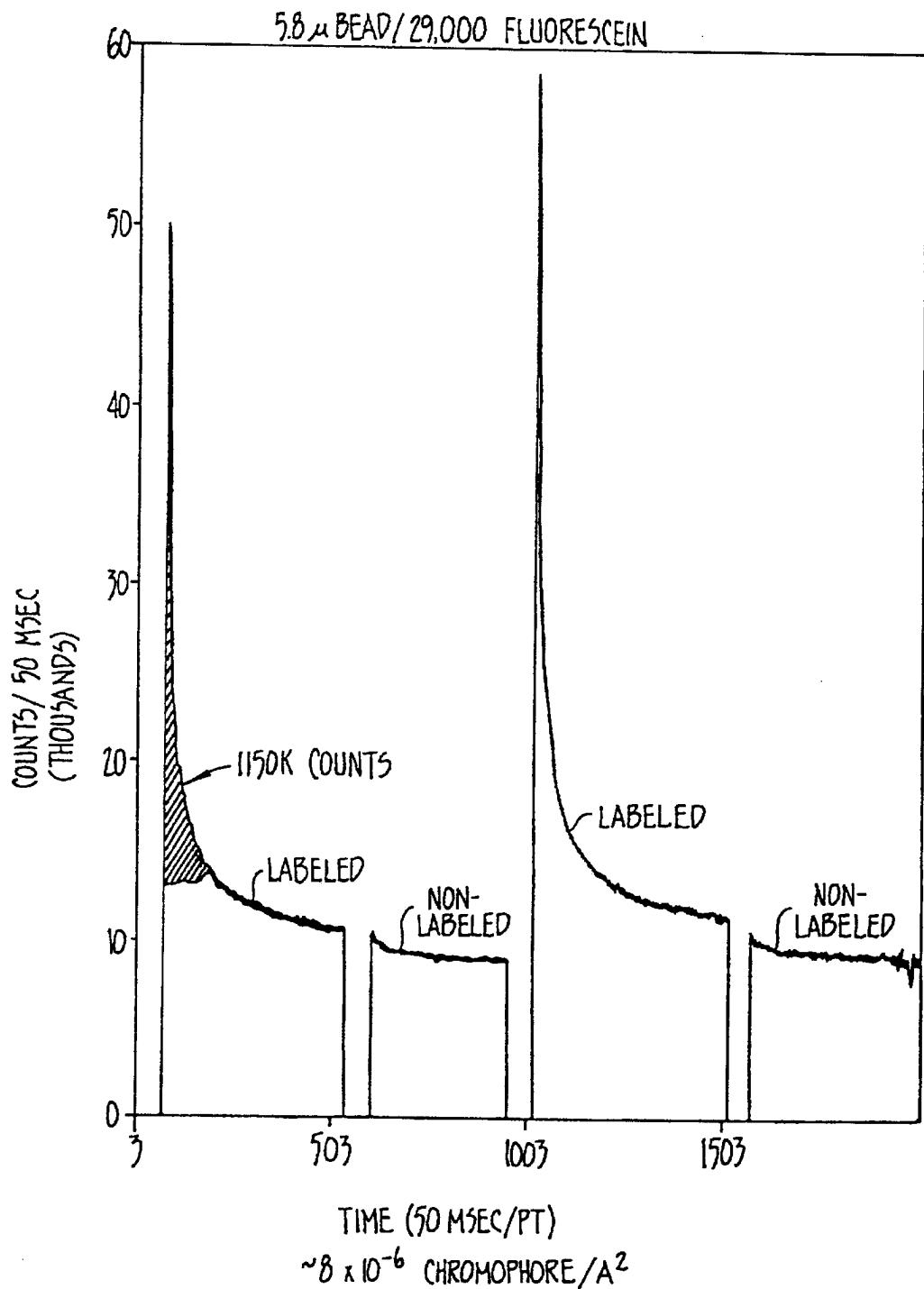


FIG. 11B.

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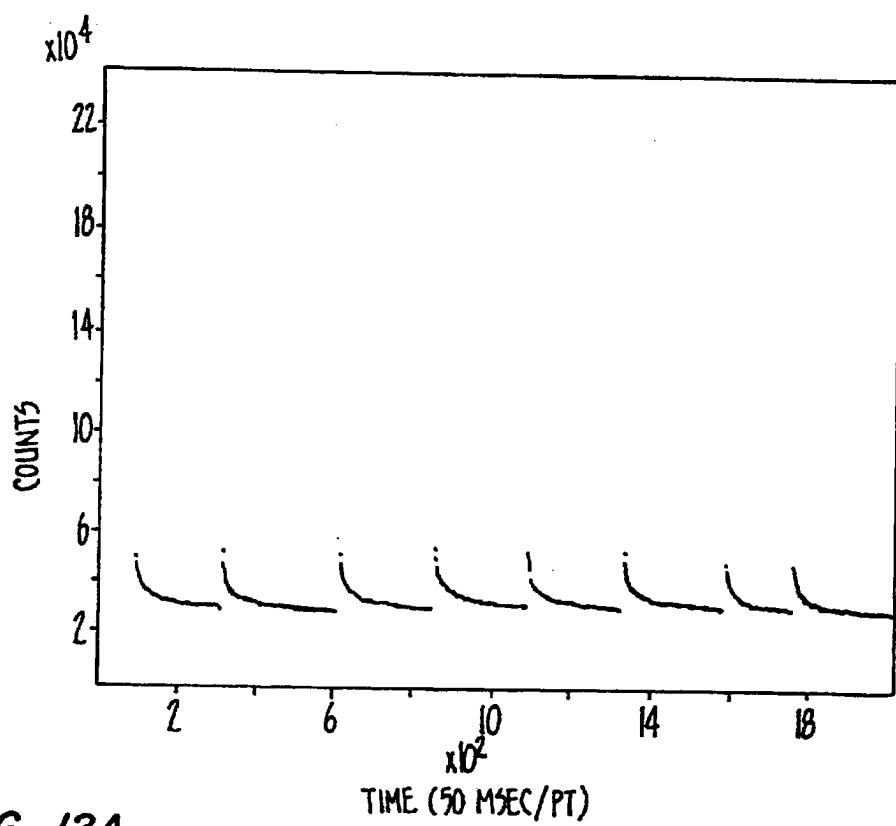


FIG. 12A.

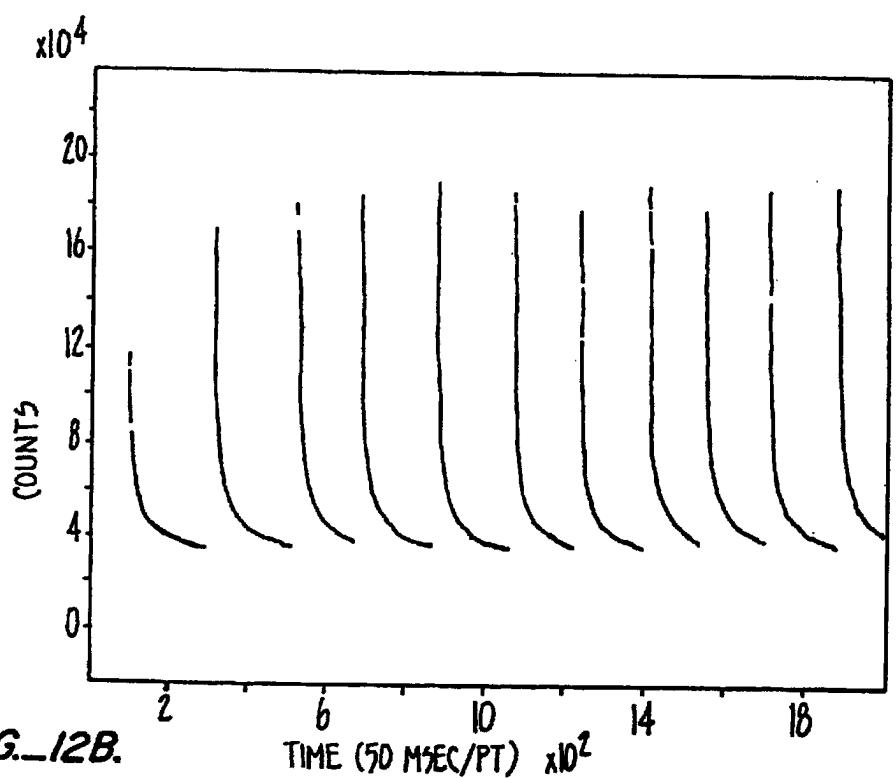


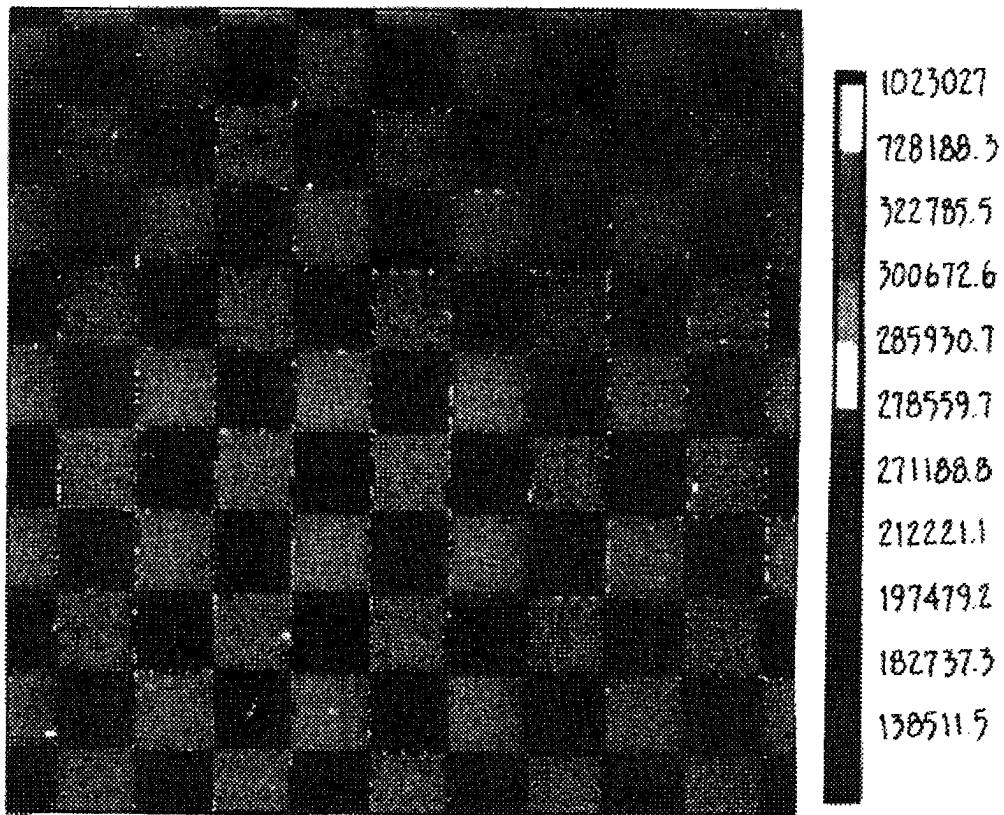
FIG. 12B.

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MEAN 285930.7
VAR: 2.173242E+10
 σ : 147419.2

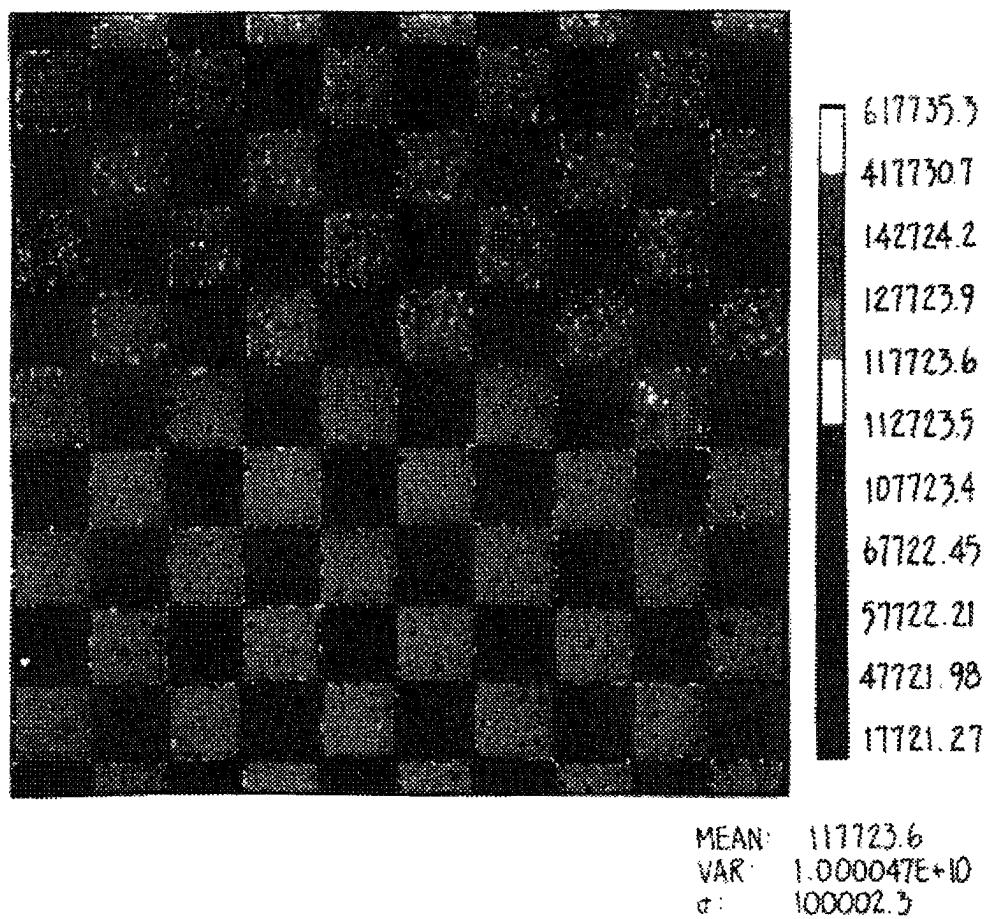
FIG. 13A.

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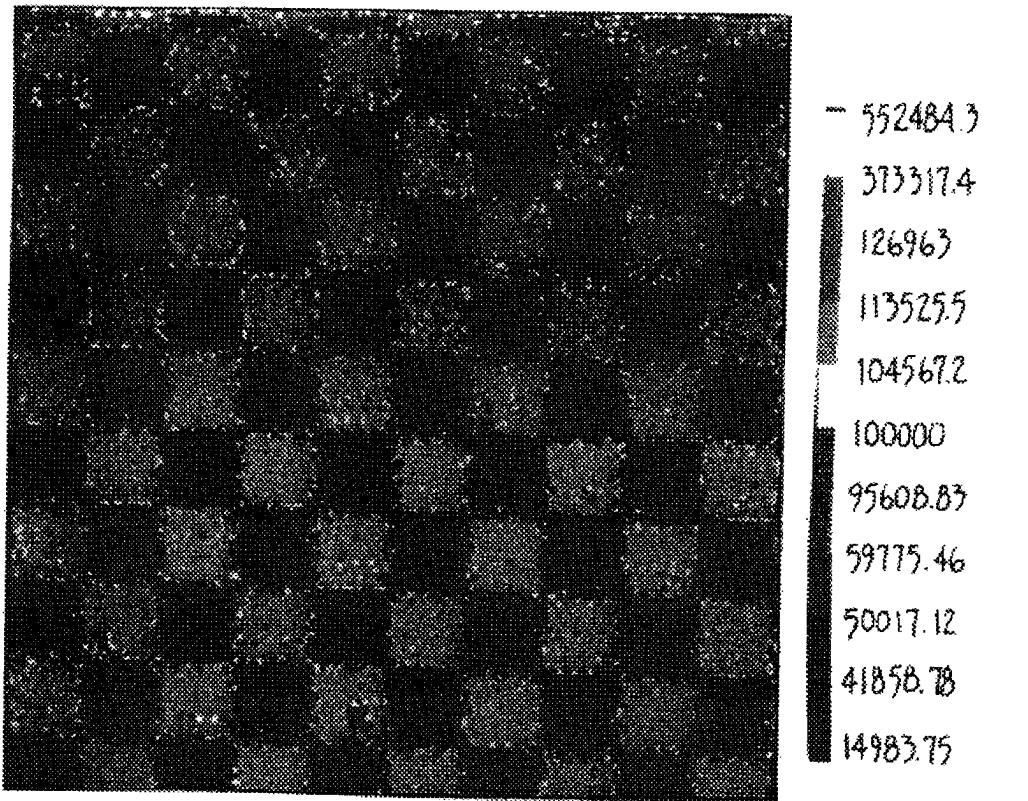
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MEAN: 117723.6
VAR: 1.000047E+10
 σ : 100002.3

FIG. 13B.

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MEAN: 104567.2
VAR: 8.025189E+09
σ: 89583.42

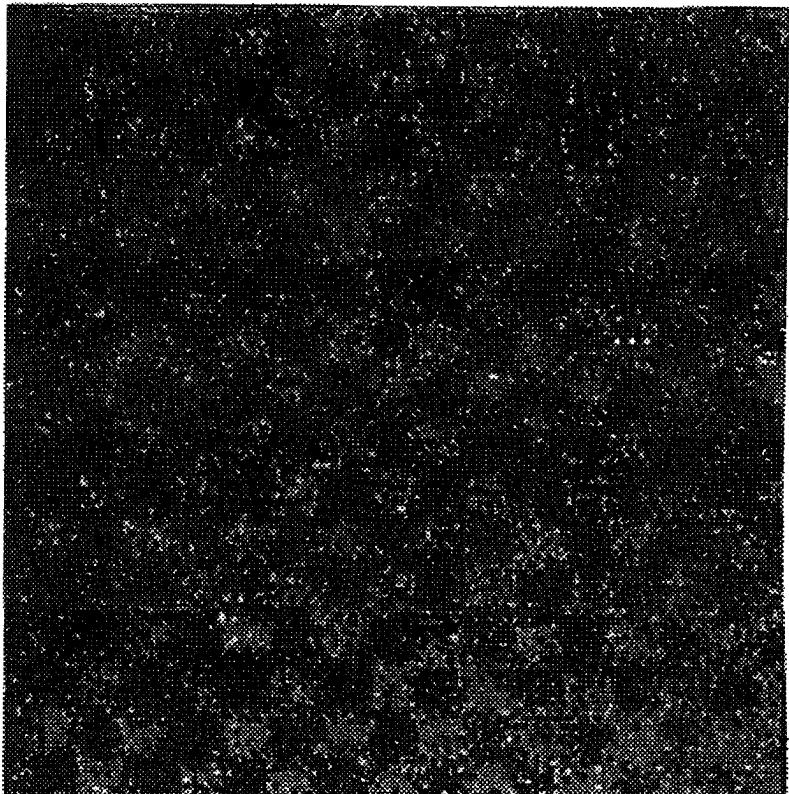
FIG. 13C.

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MEAN: 96546.92
VAR: 6.358437E+09
σ: 79739.8

FIG. 13D.

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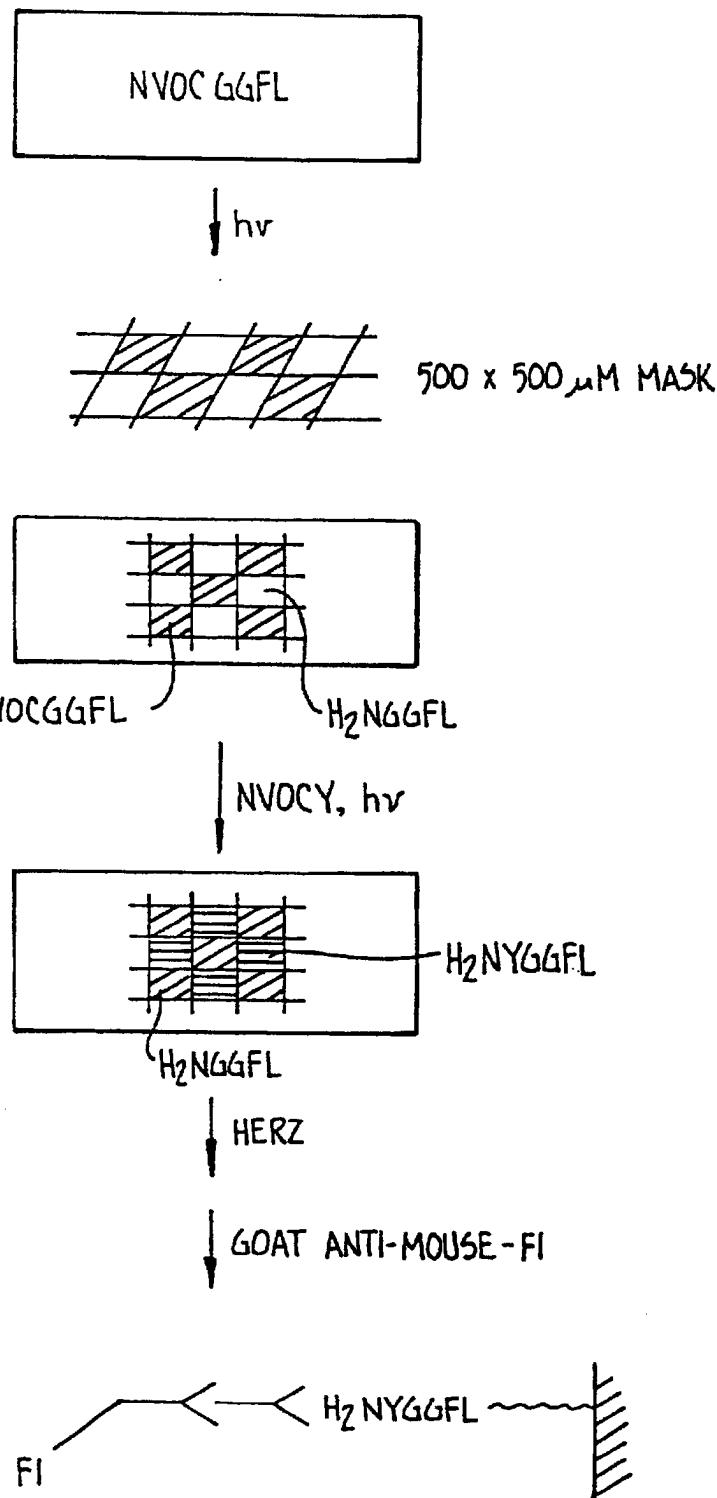


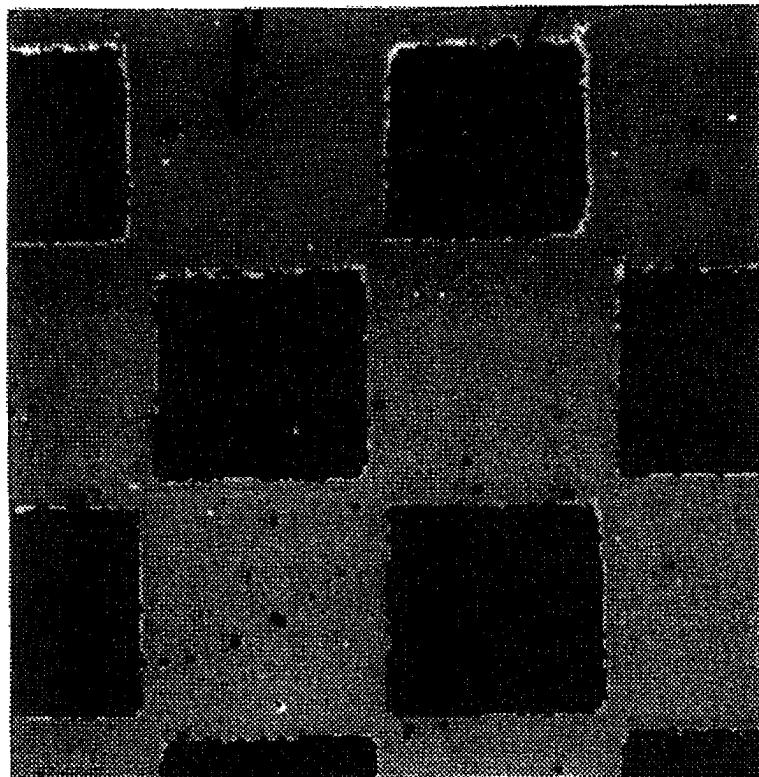
FIG. 14B.

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50780.26
34141.69
30813.97
28595.5
27486.26
26377.02
17503.12
11956.92
6410.734
-15114.03
37958.79

MEAN: 28595.5
VAR: 4.921637E+08
 σ : 22104.76

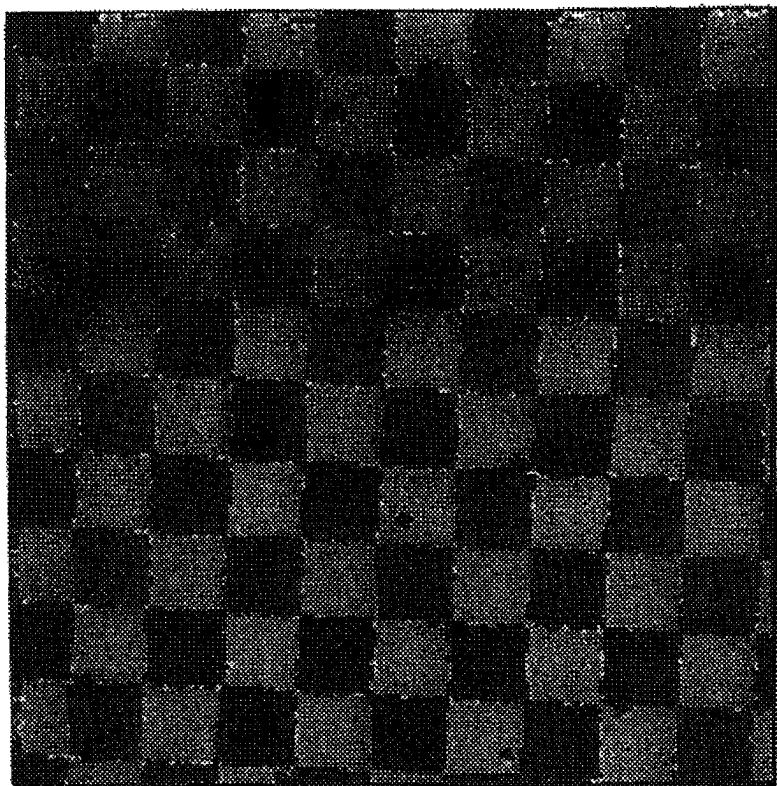
FIG. 15A.

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879976.1
6005043
216230.6
195270.2
181296.6
174309.8
167323
111428.7
97455.07
83481.48
41560.72

MEAN: 181296.6
VAR: 1.952612E+10
 σ : 139735.9

FIG. 15B.

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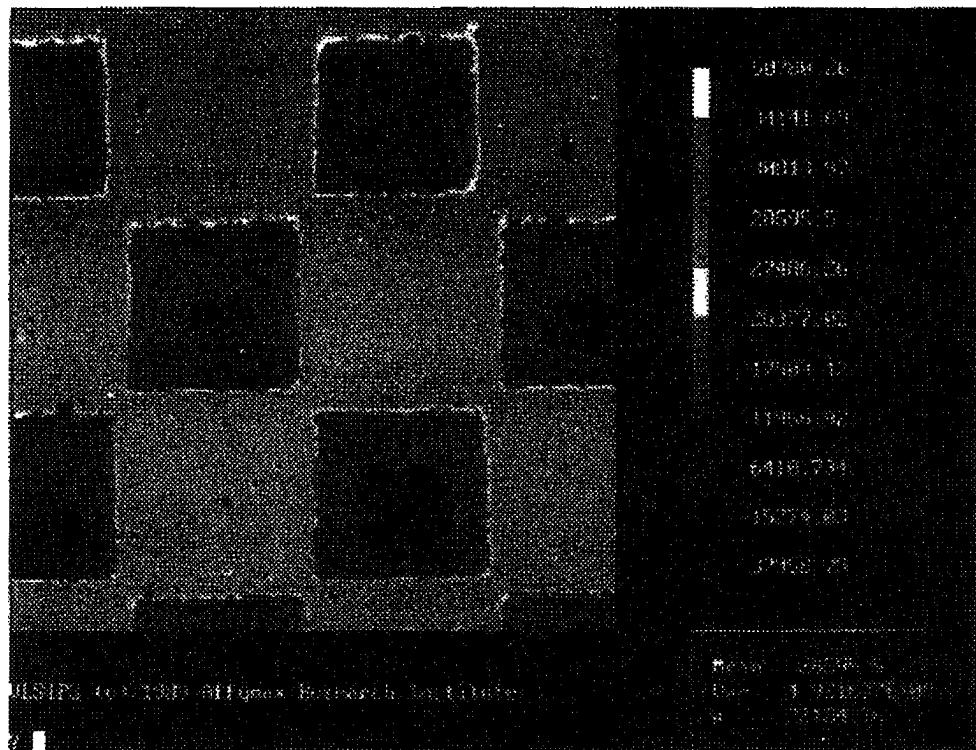


FIG. 15C

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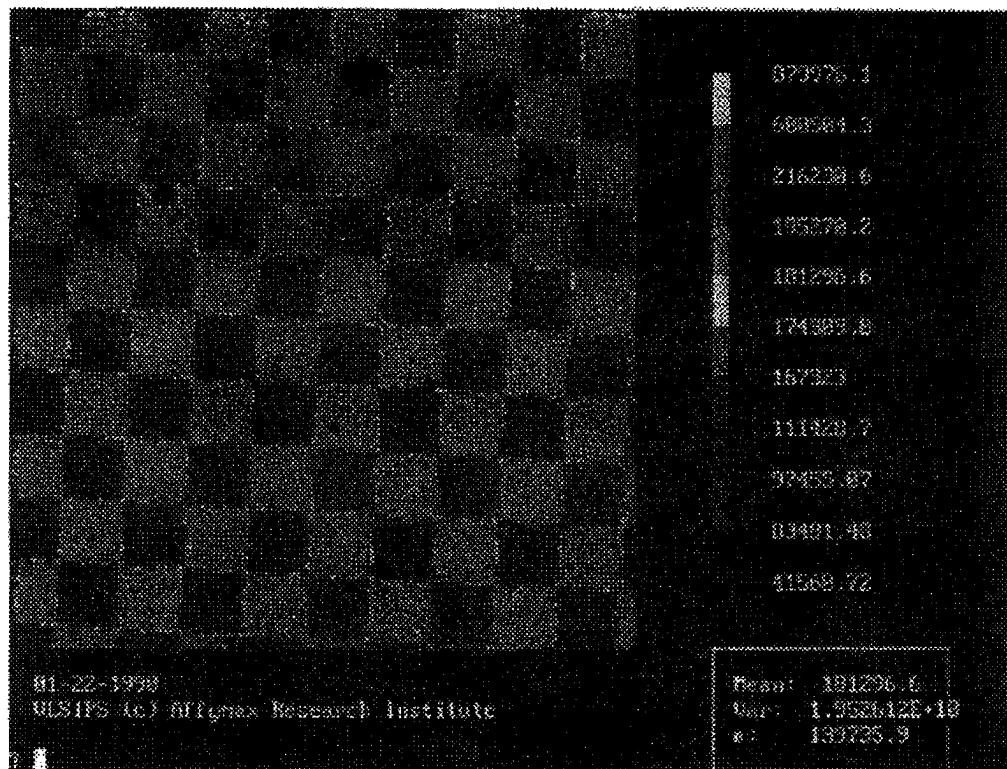


FIG. 15D

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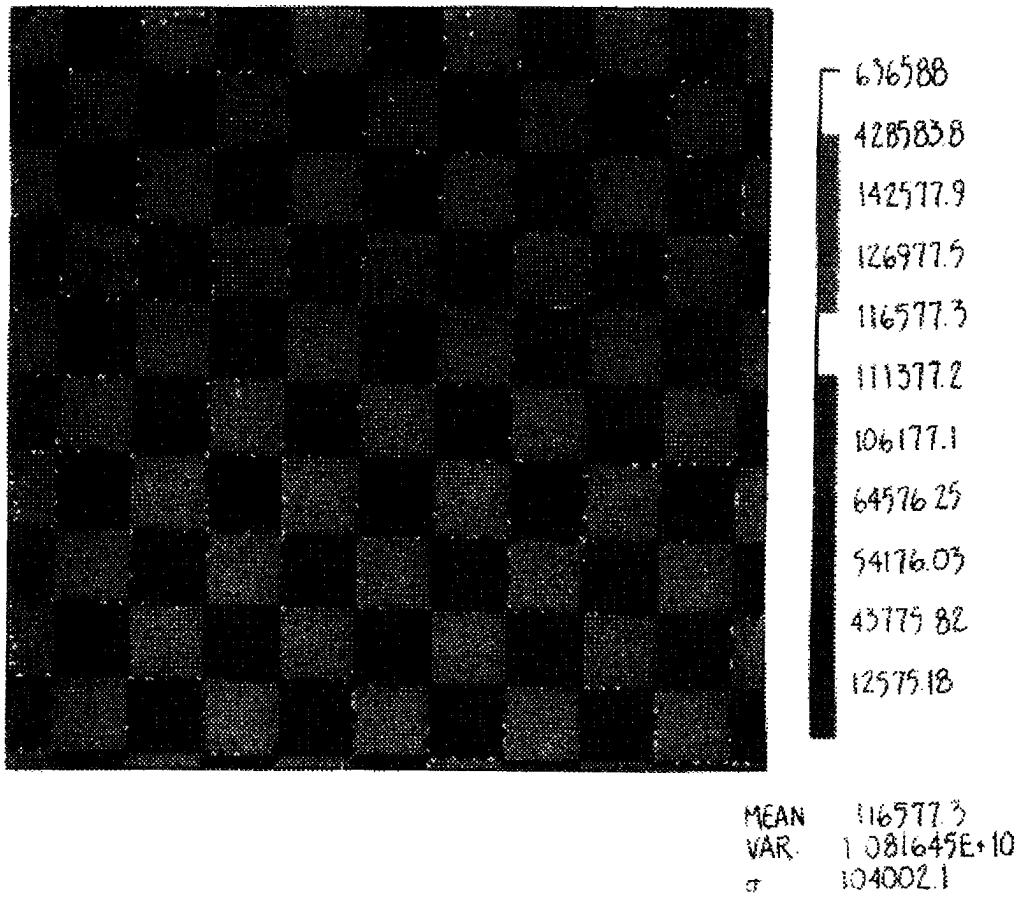
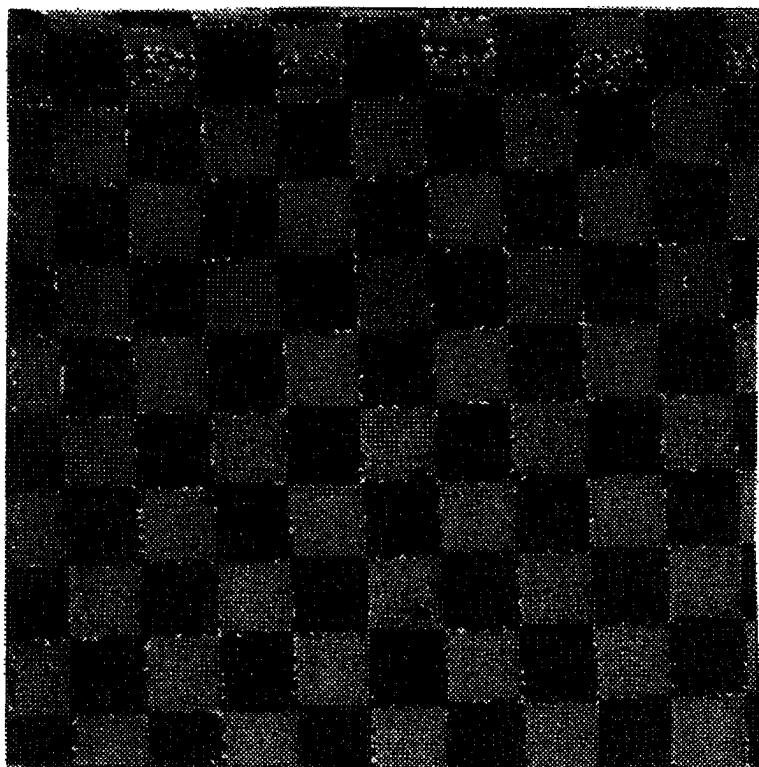


FIG. 16.

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667340.3
453053
158397
142324.9
131610.1
126252.7
120895.3
78036.29
67321.52
56606.77
24462.47

MEAN: 131610.1
VAR: 1.148062E+10
σ: 107147.6

FIG. 17.

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P A S G

<u>L</u> PGFL	<u>L</u> AGFL	<u>L</u> SGFL	<u>L</u> GGFL
<u>F</u> PGFL	<u>F</u> AGFL	<u>F</u> SGFL	<u>F</u> GGFL
<u>W</u> PGFL	<u>W</u> AGFL	<u>W</u> SGFL	<u>W</u> GGFL
<u>Y</u> PGFL	<u>Y</u> AGFL	<u>Y</u> SGFL	<u>Y</u> GGFL

L SET

FIG. 18A.

P A S G

<u>Y</u> pGFL	<u>Y</u> aGFL	<u>Y</u> sGFL	<u>Y</u> GGFL
<u>f</u> pGFL	<u>f</u> aGFL	<u>f</u> sGFL	<u>f</u> GGFL
<u>w</u> pGFL	<u>w</u> aGFL	<u>w</u> sGFL	<u>w</u> GGFL
<u>y</u> pGFL	<u>y</u> aGFL	<u>y</u> sGFL	<u>y</u> GGFL

D SET

FIG. 18B.

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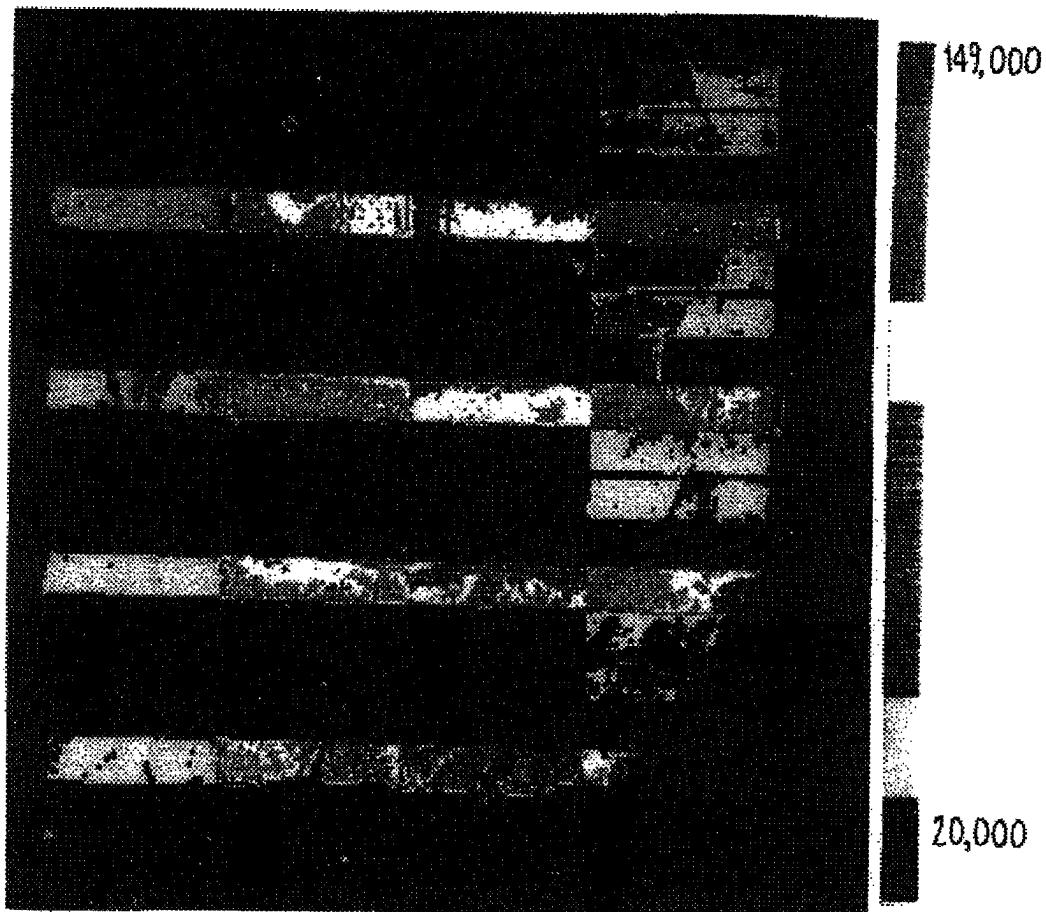


FIG. 19.

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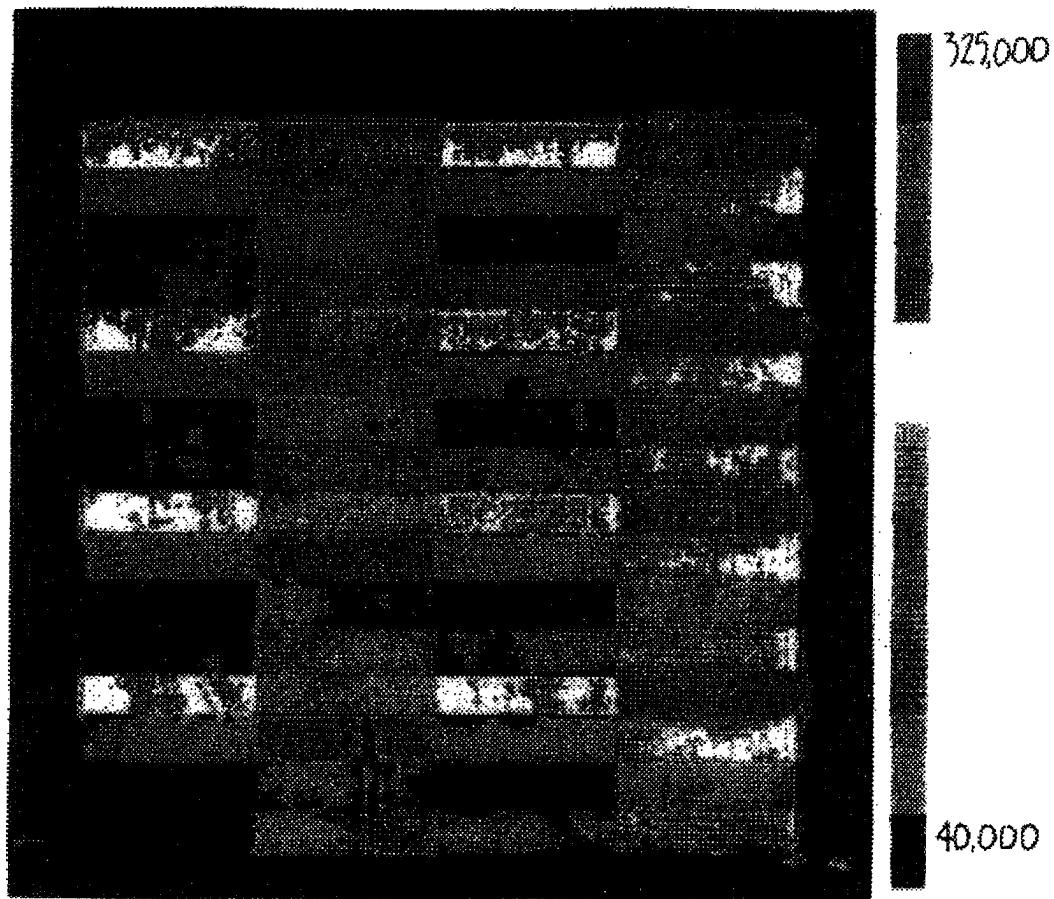


FIG. 20.

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NUCLEIC ACID READING AND ANALYSIS
SYSTEM

The present application is a continuation of and claims priority to 09/690,191 filed Oct. 16, 2000 now U.S. Pat. No. 6,403,957 which is a continuation of 09/129,470 filed Aug. 4, 1998 (U.S. Pat. No. 6,329,143) which is a continuation of 08/456,598 filed Jun. 1, 1995 (U.S. Pat. No. 6,225,625), which is a divisional of 07/954,646 filed Sep. 30, 1992 (U.S. Pat. No. 5,445,934), which is a divisional of 07/850,356 filed Mar. 12, 1992 (U.S. Pat. No. 5,405,783) which is a divisional of 07/492,462 filed Mar. 7, 1990 (U.S. Pat. No. 5,143,854), which is a continuation-in-part of 07/362,901 filed Jun. 7, 1989, now abandoned, the disclosures of which are incorporated by reference.

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BACKGROUND OF THE INVENTION

The present inventions relate to the synthesis and placement of materials at known locations. In particular, one embodiment of the inventions provides a method and associated apparatus for preparing diverse chemical sequences at known locations on a single substrate surface. The inventions may be applied, for example, in the field of preparation of oligomer, peptide, nucleic acid, oligosaccharide, phospholipid, polymer, or drug congener preparation, especially to create sources of chemical diversity for use in screening for biological activity.

The relationship between structure and activity of molecules is a fundamental issue in the study of biological systems. Structure-activity relationships are important in understanding, for example, the function of enzymes, the ways in which cells communicate with each other, as well as cellular control and feedback systems.

Certain macromolecules are known to interact and bind to other molecules having a very specific three-dimensional spatial and electronic distribution. Any large molecule having such specificity can be considered a receptor, whether it is an enzyme catalyzing hydrolysis of a metabolic intermediate, a cell-surface protein mediating membrane transport of ions, a glycoprotein serving to identify a particular cell to its neighbors, an IgG-class antibody circulating in the plasma, an oligonucleotide sequence of DNA in the nucleus, or the like. The various molecules which receptors selectively bind are known as ligands.

Many assays are available for measuring the binding affinity of known receptors and ligands, but the information which can be gained from such experiments is often limited by the number and type of ligands which are available. Novel ligands are sometimes discovered by chance or by application of new techniques for the elucidation of molecular structure, including x-ray crystallographic analysis and recombinant genetic techniques for proteins.

Small peptides are an exemplary system for exploring the relationship between structure and function in biology. A peptide is a sequence of amino acids. When the twenty naturally occurring amino acids are condensed into polymeric molecules they form a wide variety of three-

2

dimensional configurations, each resulting from a particular amino acid sequence and solvent condition. The number of possible pentapeptides of the 20 naturally occurring amino acids, for example, is 20^5 or 3.2 million different peptides. The likelihood that molecules of this size might be useful in receptor-binding studies is supported by epitope analysis studies showing that some antibodies recognize sequences as short as a few amino acids with high specificity. Furthermore, the average molecular weight of amino acids puts small peptides in the size range of many currently useful pharmaceutical products.

Pharmaceutical drug discovery is one type of research which relies on such a study of structure-activity relationships. In most cases, contemporary pharmaceutical research can be described as the process of discovering novel ligands with desirable patterns of specificity for biologically important receptors. Another example is research to discover new compounds for use in agriculture, such as pesticides and herbicides.

Sometimes, the solution to a rational process of designing ligands is difficult or unyielding. Prior methods of preparing large numbers of different polymers have been painstakingly slow when used at a scale sufficient to permit effective rational or random screening. For example, the "Merrifield" method (*J. Am. Chem. Soc.* (1963) 85:2149-2154, which is incorporated herein by reference for all purposes) has been used to synthesize peptides on a solid support. In the Merrifield method, an amino acid is covalently bonded to a support made of an insoluble polymer. Another amino acid with an alpha protected group is reacted with the covalently bonded amino acid to form a dipeptide. After washing, the protective group is removed and a third amino acid with an alpha protective group is added to the dipeptide. This process is continued until a peptide of a desired length and sequence is obtained. Using the Merrifield method, it is not economically practical to synthesize more than a handful of peptide sequences in a day.

To synthesize larger numbers of polymer sequences, it has also been proposed to use a series of reaction vessels for polymer synthesis. For example, a tubular reactor system may be used to synthesize a linear polymer on a solid phase support by automated sequential addition of reagents. This method still does not enable the synthesis of a sufficiently large number of polymer sequences for effective economical screening.

Methods of preparing a plurality of polymer sequences are also known in which a foraminous container encloses a known quantity of reactive particles, the particles being larger in size than foramina of the container. The containers may be selectively reacted with desired materials to synthesize desired sequences of product molecules. As with other methods known in the art, this method cannot practically be used to synthesize a sufficient variety of polypeptides for effective screening.

Other techniques have also been described. These methods include the synthesis of peptides on 96 plastic pins which fit the format of standard microtiter plates. Unfortunately, while these techniques have been somewhat useful, substantial problems remain. For example, these methods continue to be limited in the diversity of sequences which can be economically synthesized and screened.

From the above, it is seen that an improved method and apparatus for synthesizing a variety of chemical sequences at known locations is desired.

SUMMARY OF THE INVENTION

An improved method and apparatus for the preparation of a variety of polymers is disclosed.